

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2004, 00:12:59 ; Search time 301.968 seconds
(without alignments)
10354.322 Million cell updates/sec

Title: US-09-006-627-3

Perfect score: 736
Sequence: 1 ATTACGTTTGTGATCGTA.....TTAAATTTGATTTTCTA 736

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N.Geneseq_29Jan04:*

1: Geneseqn1980s:*\n2: Geneseqn1990s:*\n3: Geneseqn2000s:*\n4: Geneseqn2001s:*\n5: Geneseqn2001bs:*\n6: Geneseqn2002s:*\n7: Geneseqn2003s:*\n8: Geneseqn2003bs:*\n9: Geneseqn2003cs:*\n10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	736	2	AAT72328 Staphyloc
2	736	100.0	736	2	AAX90602 Cognate r
3	736	100.0	2201	2	AAX90601 Histidine
4	726	98.6	1440	2	AAY75036 Staphyloc
5	657	89.3	657	7	ACF74591 Staphyloc
6	406.4	55.2	3099	4	AAH54422 S. epider
7	401.8	54.6	669	6	ABN90912 Staphyloc
8	390.4	53.0	3230	4	AAH54308 S. epider
9	347	47.1	3018	4	AAH54320 S. epider
10	302.6	41.1	501	4	AAH53697 S. epider
11	302.6	41.1	501	4	AAH53697 S. epider
12	224.8	30.5	110000	6	ABO67195-3
13	224.8	30.5	110000	6	ABO67195-3
14	202.2	27.5	110000	6	ABA03041_13
15	202.2	27.5	110000	6	ABA03041_13
16	193.6	26.3	110000	6	ABN71527_15
17	193.6	26.3	110000	6	ABN71527_15
18	193	26.2	687	6	ABN68466 Streptoc
19	193	26.2	1908	6	AAH12964 Enterococ
20	187.2	25.4	1908	6	ABN98759 Enterococ
21	187.2	25.4	687	9	ADG93255 E. faeciu
22	184.2	25.0	110000	6	ABO69245_13
23	173.8	23.6	684	6	ABN67673 Streptoc

24	165.6	22.5	110000	8	ADB12064_08	Continuation (9 of
25	161	21.9	705	8	ADB09375	ADB09375 Allotococ
26	149.8	20.4	741	6	ABN90875	ABN90875 Staphyloc
27	146.6	19.9	672	6	ABN67082	ABN67082 Streptoc
28	144	18.9	684	6	ADA32762	ADA32762 DNA encod
29	138.8	18.6	110000	6	ABA90521_17	Continuation (18 o
30	137.6	18.7	110000	6	ABO69245_20	Continuation (21 o
31	137.2	18.6	110000	6	ABN71527_20	Continuation (21 o
32	135.6	18.4	741	7	ACF72642	ACF72642 Staphyloc
33	131.8	17.9	690	7	ACA29466	ACA29466 Prokaryot
34	131	17.8	110000	6	ABN71527_06	Continuation (7 of
35	130.2	17.7	708	6	ABN66633	ABN66633 Streptoc
36	130	17.7	31517	2	AAH13117	AAH13117 Enterococ
37	130	17.7	31517	6	ABN98912	ABN98912 Enterococ
38	128	17.4	1037	6	ABO70350	ABO70350 Listeria
39	127.4	17.3	900	2	AAT72329	AAT72329 Staphyloc
40	126.4	17.2	717	6	ABO68073	ABO68073 Listeria
41	126.4	17.2	110000	6	ABN71527_09	Continuation (10 o
42	126.4	17.2	110000	6	ABA03041_10	Continuation (11 o
43	126.4	17.2	110000	6	ABA03041_20	Continuation (21 o
44	125.8	17.1	12022	2	AAH13054	AAH13054 Enterococ
45	125.8	17.1	12022	6	ABN98849	ABN98849 Enterococ

ALIGNMENTS

RESULT 1	
AA72328	AA72328 standard; cDNA, 736 BP.
AC	AA72328;
DT	17-OCT-2003 (revised)
DT	16-JAN-1998 (first entry)
DE	Staphylococcus aureus encoding a novel response regulator protein.
XX	
XX	Antibacterial; anti-Staphylococcus; gene therapy; bacterial infection;
KW	prophylaxis; two component signal transduction system; TCSTS; Resd;
KW	response regulator; Staphylococcus; Bacillus; vaccine; wound treatment;
XX	dental; surgery; antibody; ds.
OS	Staphylococcus aureus; WCUR29.
XX	
XX	Key
FT	Location/Qualifiers
FT	complement (13..672)
FT	/*tag= a
FT	/product= "response_regulator_protein"
XX	
XX	W09723506-A1.
XX	
XX	03-JUL-1997.
XX	
XX	20-DEC-1996; 96WO-GB003261.
XX	
XX	22-DEC-1995; 95GB-00026359.
XX	
XX	(SMIK) SMITHKLINE BEECHAM PLC.
XX	
XX	Wallis N, Hodgson JE;
XX	
XX	WPI, 1997-350970/32.
XX	
XX	P-FSDB; AAW19274.
XX	
XX	Isolated nucleic acid encoding Staphylococcus aureus response regulator -
XX	useful to treat or prevent bacterial infections, in vaccines and for
XX	diagnosis.
XX	
XX	Claim 4; Page 45-46; 59pp; English.
XX	
XX	The present sequence represents a polynucleotide, encoding a novel
XX	response regulator protein from Staphylococcus aureus. DNA was isolated

CC from a chromosomal library of NCIMB 40771. The encoded polypeptide is a
 CC response regulatory component of the bacterial two component signal
 CC transduction system (TCSTS), related to the Resd protein of *Bacillus*
 CC subtilis (42% identity). Inhibition of the polypeptide prevents the
 CC bacteria from establishing or maintaining infection by preventing them
 CC from producing the factors necessary for pathogenesis. The present DNA
 CC can be used to produce recombinant polypeptides in vivo and in gene
 CC therapy. The antagonist and agonists can also be used to inhibit
 CC bacterial infection. Typical applications are in wound treatment (to
 CC prevent bacterial adherence), prophylaxis in dental or other surgery (as
 CC an alternative or adjunct to antibiotic therapy) or for treating in-
 CC dwelling devices immediately before insertion. Detection of the present
 CC polynucleotide or the polypeptide, by usual hybridisation or
 CC immunosays, can be used to diagnose infection. Elevated levels of
 CC expression would indicate bacterial infection. The polypeptide can also
 CC be used in protective vaccines to induce antibody production. The
 CC antibodies themselves can be used as a diagnostic reagent or as a
 CC therapeutic antagonist. (Updated on 17-OCT-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 736 BP; 213 A; 138 C; 97 G; 288 T; 0 U; 0 Other;

Query Match 100.0%; Score 736; DB 2; Length 736;
 Best Local Similarity 100.0%; Pred. No. 2e-157;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTTAGCTTTGTCATCGTATCAATACCCAGCCAGCAAGCTTTCAATCTTTGTC 60
 DB 1 ATTTAGCTTTGTCATCGTATCAATACCCAGCCAGCAAGCTTTCAATCTTTGTC 60
 QY 61 ACGATCGTATGTTTAACTTTGCTGTAATATCTTAATAAACAATCAACGATTTGT 120
 DB 61 ACGATCGTATGTTTAACTTTGCTGTAATATCTTAATAAACAATCAACGATTTGT 120
 QY 121 TTCTACTTCACTATATATACCCATATGATTTAAATTTGTCGGTGCATACATG 180
 DB 121 TTCTACTTCACTATATATACCCATATGATTTAAATTTGTCGGTGCATACATG 180
 QY 181 GTTTTATTTTACGTCAGATATAGTAAATCACTGTTTTGTTTAAATCAATTC 240
 DB 181 GTTTTATTTTACGTCAGATATAGTAAATCACTGTTTTGTTTAAATCAATTC 240
 QY 241 TGGGCGCATTTACCGTCATCTTAAAGCGTCTTATCAATTTGAATACCGTGCATCAT 300
 DB 241 TGGGCGCATTTACCGTCATCTTAAAGCGTCTTATCAATTTGAATACCGTGCATCAT 300
 QY 301 AATATCTTTTGGCTGACGAGATTAATGCAAGATTTGCTTAAAGTTCTTCAAT 360
 DB 301 AATATCTTTTGGCTGACGAGATTAATGCAAGATTTGCTTAAAGTTCTTCAAT 360
 QY 361 ATCAAAGCGCTTAATATATATGCTGACCGTATCAAGCCGCAACTTTGTCAT 420
 DB 361 ATCAAAGCGCTTAATATATATGCTGACCGTATCAAGCCGCAACTTTGTCAT 420
 QY 421 CGTATCACTTTTGGCTGATTAATATGATAGGTGATGTTGTTGTTCAATTTGGC 480
 DB 421 CGTATCACTTTTGGCTGATTAATATGATAGGTGATGTTGTTGTTCAATTTGGC 480
 QY 481 ACAATTTTCAAGCCATTAATTTGACGCAATTAATCTTAATATGATTAATCAATAGTA 540
 DB 481 ACAATTTTCAAGCCATTAATTTGACGCAATTAATCTTAATATGATTAATCAATAGTA 540
 QY 541 ATGAGCTAAGCGCTTTATCTAAACCGTCTTGCATCATPACTGTTGCCAATTTAAT 600
 DB 541 ATGAGCTAAGCGCTTTATCTAAACCGTCTTGCATCATPACTGTTGCCAATTTAAT 600
 QY 601 TTGATGTGAGTTCATTAAGAAATCTGCTAAAGTTTGTCTCAATCTTCAATTA 660
 DB 601 TTGATGTGAGTTCATTAAGAAATCTGCTAAAGTTTGTCTCAATCTTCAATTA 660
 QY 661 AATTGGTATTTGATACCATCATATAGACTTTTCTTAATTAAGTAATATATTTTAA 720
 DB 661 AATTGGTATTTGATACCATCATATAGACTTTTCTTAATTAAGTAATATATTTTAA 720

QY 721 ATTTGATATTTCTTA 736
 DB 721 ATTTGATATTTCTTA 736

RESULT 2
 AAX90602
 ID AAX90602 standard; DNA; 736 BP.
 XX
 AC AAX90602;
 XX

DT 01-OCT-1999 (first entry)
 XX

DE Cognate response regulator, polynucleotide, of Histidine kinase.

KW Cognate response regulator; Two component signal transduction system;
 TCSTS; Histidine kinase; virulence; bacterial pathogenesis; screening;
 KW autophosphorylate; antibacterial agent; *Helicobacter pylori*; ds.
 XX

OS *Staphylococcus aureus*.

Key Location/Qualifiers
 CDS complement(13..672)
 FT /tag= a
 FT /product= "Cognate response regulator to histidine
 FT kinase"
 FT /note= "shows 42% identity to Resd response regulator
 FT protein from *Bacillus subtilis*"

PN W09936508-A1.
 PD 22-JUL-1999.

PF 12-JAN-1999; 99WO-US000610.
 XX

PR 13-JAN-1998; 98US-00006627.
 XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

PI Wallis NG, Shilling LK, Mooney JL, Debouck C, Zhong Y;
 PI Jaworski DD, Wang M, Throup JP;
 XX

DR WPI; 1999-444390/37.
 DR P-PSDB; AAY28602.
 XX

PT Novel histidine kinase polynucleotides and polypeptides used to screen
 for antibacterial compounds.
 XX

PS Claim 24; Page 7; 43pp; English.

CC The present polynucleotide sequence encodes the *Staphylococcus aureus*
 CC response regulator cognate to histidine kinase. Histidine kinase is a
 CC component of the two component signal transduction systems (TCSTS) which
 CC is involved in bacterial pathogenesis and virulence. It undergoes
 CC autophosphorylation at a histidine residue and the phosphate group is
 CC transferred to the cognate response regulator. This novel response
 CC regulator shows 42% identity to the Resd response regulator protein from
 CC *Bacillus subtilis*. The cognate response regulator can be used for
 CC screening drugs which interfere with the interaction of histidine kinase
 CC and the response regulator. The histidine kinase products can be used to
 CC screen and identify new antibacterial drugs, agonists and antagonists
 CC effective against *Helicobacter pylori* infections and infections caused by
 CC resistant *S. aureus* strains
 CC
 XX

SQ Sequence 736 BP; 213 A; 138 C; 97 G; 288 T; 0 U; 0 Other;

Query Match 100.0%; Score 736; DB 2; Length 736;
 Best Local Similarity 100.0%; Pred. No. 2e-157;
 Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTTAGCTTTGTCATCGTATCAATACCCAGCCAGCAAGCTTTCAATCTTTGTC 60
 DB 1 ATTTAGCTTTGTCATCGTATCAATACCCAGCCAGCAAGCTTTCAATCTTTGTC 60

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OM protein - protein search, using sw model

Run on: October 4, 2004, 18:03:18 ; Search time 16.0164 Seconds
(without alignments)
705.906 Million cell updates/sec

Title: US-09-006-627-4

Perfect score: 1122

Sequence: 1 MTQILIVEDONLAFLELE.....KPYDRDKMETVGVYIR 219

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1132	100.0	219	3	US-08-771-110-2
2	1122	100.0	219	4	US-09-642-000-4
3	968	86.3	222	4	US-09-134-001C-3212
4	654	58.3	228	4	US-09-107-532A-6536
5	468.5	41.8	234	4	US-09-634-238-220
6	458	40.8	246	4	US-09-107-532A-4135
7	452	40.3	246	4	US-09-134-001C-3175
8	449.5	40.1	234	4	US-09-107-532A-6746
9	449	40.0	233	4	US-09-082-077-4
10	449	40.0	234	4	US-09-134-001C-3063
11	449	40.0	239	4	US-08-956-171E-5239
12	442	39.4	234	1	US-08-850-118-2
13	442	39.4	234	2	US-09-008-253-2
14	442	39.4	234	3	US-09-093-335-2
15	442	39.4	245	4	US-09-134-001C-3179
16	435.5	38.8	245	4	US-09-252-991A-31392
17	435	38.8	184	4	US-09-134-000C-3820
18	432.5	38.5	234	3	US-08-771-321-2
19	430.5	38.4	231	4	US-09-134-000C-5664
20	429	38.2	227	4	US-09-111-164-367
21	425	37.9	231	2	US-08-286-819A-12
22	425	37.9	231	2	US-08-286-819A-43
23	425	37.9	231	3	US-08-980-357-12
24	425	37.9	231	3	US-08-980-357-43
25	425	37.9	231	3	US-08-980-357-12
26	425	37.9	231	3	US-08-980-357-43
27	425	37.9	2296	3	US-08-286-819A-27
					Sequence 27, Appl

28	424	37.8	230	4	US-09-543-681A-6135	Sequence 6135, Ap
29	421	37.5	267	4	US-09-252-991A-26894	Sequence 26894, A
30	419.5	37.4	241	4	US-09-107-532A-4846	Sequence 4846, Ap
31	419	37.3	264	4	US-09-489-039A-10454	Sequence 10454, A
32	418.5	37.3	236	4	US-09-107-532A-6873	Sequence 6873, Ap
33	416.5	37.1	231	4	US-09-134-000C-5145	Sequence 5145, Ap
34	413.5	36.9	229	4	US-09-252-991A-24389	Sequence 24389, A
35	413	36.8	244	4	US-09-252-991A-25108	Sequence 25108, A
36	410.5	36.6	269	4	US-09-634-238-222	Sequence 222, App
37	406	36.2	229	2	US-08-286-819A-45	Sequence 45, Appl
38	406	36.2	229	3	US-08-980-357-45	Sequence 45, Appl
39	404	36.0	230	4	US-09-252-991A-20963	Sequence 20963, A
40	403.5	36.0	243	2	US-08-771-455-2	Sequence 2, Appl1
41	401.5	35.8	249	4	US-09-328-352-4690	Sequence 4690, Ap
42	399	35.6	230	4	US-09-489-039A-13339	Sequence 13339, A
43	397.5	35.4	227	4	US-09-107-532A-6769	Sequence 6769, Ap
44	394.5	35.2	237	4	US-09-252-991A-30493	Sequence 30493, A
45	394	35.1	236	4	US-09-489-039A-11254	Sequence 11254, A

ALIGNMENTS

RESULT 1
; Sequence 2, Application US/08771110
; Patent No. 6084086
GENERAL INFORMATION:
APPLICANT: Wallis, Nicola G.
APPLICANT: Hodgson, John E.
TITLE OF INVENTION: No. 6084086e1 Compounds
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,110
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31316
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
; US-08-771-110-2
Query Match 100.0%; Score 1122; DB 3; Length 219;
Best Local Similarity 100.0%; Pred. No. 5.1e-111;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTQILIVEDONLAFLELETHENVNVDREYDQDGLKLSHYDDIILDMIPSG 60
DB 1 MTQILIVEDONLAFLELETHENVNVDREYDQDGLKLSHYDDIILDMIPSG 60
QY 61 LEICRKIRQOQSTPIIITAKSDTYDKVAGLDYGVADYIVFPDIEELARIRAIRLRQ 120

Db 61 LEICRKIRQOOSTPIIIITAKSDTYDKVAGLDYGADYIVKPFIDIELLARIIRARROP 120
QY 121 OKDIIDVNGITIDKNAFKYTVNGAEIELTKTEYDLYLLAENKNHWOREQIINHVGYN 180
Db 121 OKDIIDVNGITIDKNAFKYTVNGAEIELTKTEYDLYLLAENKNHWOREQIINHVGYN 180
QY 181 SEVETNVVDYIRIRLNKLPYDRDKMIETVRGVYIR 219
Db 181 SEVETNVVDYIRIRLNKLPYDRDKMIETVRGVYIR 219

RESULT 2
US-09-642-000-4

Sequence 4, Application US/09642000
Patent No. 6548281
GENERAL INFORMATION:
APPLICANT: Wallis, Nicola G.
Shilling, Lisa K.
Mooney, Jeffrey L.
Debouck, Christine
Zhong, Yiyi
Jaworski, Deborah D.
Wang, Min
Throup, John P.
TITLE OF INVENTION: Histidine Kinase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/642.000
FILING DATE: 18-AUG-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/006.627
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36.795
REFERENCE/DOCKET NUMBER: GMI0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2468
TELEFAX: 215-994-2222
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-642-000-4

Query Match 100.0%; Score 1122; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 5.1e-111;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTOIILVEDEQNIAEELTHEYNTVDTEYDGGDLKALSHYVDLIIDMLPSSING 60
Db 1 MTOIILVEDEQNIAEELTHEYNTVDTEYDGGDLKALSHYVDLIIDMLPSSING 60
QY 61 LEICRKIRQOOSTPIIIITAKSDTYDKVAGLDYGADYIVKPFIDIELLARIIRARROP 120

Db 61 LEICRKIRQOOSTPIIIITAKSDTYDKVAGLDYGADYIVKPFIDIELLARIIRARROP 120
QY 121 OKDIIDVNGITIDKNAFKYTVNGAEIELTKTEYDLYLLAENKNHWOREQIINHVGYN 180
Db 121 OKDIIDVNGITIDKNAFKYTVNGAEIELTKTEYDLYLLAENKNHWOREQIINHVGYN 180
QY 181 SEVETNVVDYIRIRLNKLPYDRDKMIETVRGVYIR 219
Db 181 SEVETNVVDYIRIRLNKLPYDRDKMIETVRGVYIR 219

RESULT 3
US-09-134-001C-3212

Sequence 3212, Application US/0913401C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134.001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064.964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055.779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3212
LENGTH: 222
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3212

Query Match 86.3%; Score 968; DB 4; Length 222;
Best Local Similarity 84.5%; Pred. No. 1.1e-94;
Matches 185; Conservative 21; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTOIILVEDEQNIAEELTHEYNTVDTEYDGGDLKALSHYVDLIIDMLPSSING 60
Db 4 MTOIILVEDEQNIAEELTHEYNTVDTEYDGGDLKALSKPYDLYLLDMLPSSING 63
QY 61 LEICRKIRQOOSTPIIIITAKSDTYDKVAGLDYGADYIVKPFIDIELLARIIRARROP 120
Db 64 LEICRKIRQOOSTPIIIITAKSDTYDKVAGLDYGADYIVKPFIDIELLARIIRARROP 123
QY 121 OKDIIDVNGITIDKNAFKYTVNGAEIELTKTEYDLYLLAENKNHWOREQIINHVGYN 180
Db 124 OKDIIDVNGITIDKNAFKYTVNGAEIELTKTEYDLYLLAENKNHWOREQIINHVGYN 183
QY 181 SEVETNVVDYIRIRLNKLPYDRDKMIETVRGVYIR 219
Db 184 SEVETNVVDYIRIRLNKLPYDRDKMIETVRGVYIR 222

RESULT 4
US-09-107-532A-6536

Sequence 6536, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE/ GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Walham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC

QY 1 MTOIILVEDEQNIAEELTHEYNTVDTEYDGGDLKALSHYVDLIIDMLPSSING 60
Db 1 MTOIILVEDEQNIAEELTHEYNTVDTEYDGGDLKALSHYVDLIIDMLPSSING 60
QY 61 LEICRKIRQOOSTPIIIITAKSDTYDKVAGLDYGADYIVKPFIDIELLARIIRARROP 120